



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/730,478

Source:

OIPF

Date Processed by STIC:

2/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

### Raw Sequence Listing Error Summary

### SUGGESTED CORRECTION

**SERIAL NUMBER:**

SERIAL NUMBER: 09/730478

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1** \_\_\_\_\_ Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2** \_\_\_\_\_ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3** \_\_\_\_\_ Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4** ✓ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5** \_\_\_\_\_ Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6** \_\_\_\_\_ PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7** \_\_\_\_\_ Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8** \_\_\_\_\_ Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9** \_\_\_\_\_ Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10** \_\_\_\_\_ Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11** \_\_\_\_\_ Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12** \_\_\_\_\_ PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13** \_\_\_\_\_ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

SEQUENCE LISTING

5 <110> John Mundy  
Anders Boegh Jensen  
Morten Petersen  
Henrik Naestved  
Peter Brodersen

10 <120> Method of using Arabidopsis MAPK4 and  
orthologues thereof to control plant disease and plant size

15 <130> 23580 PC 1

<140> PCT/DK00/00674  
<141> 2000-12-06

20 <150> PA 1999 01746  
<151> 1999-12-06

<150> US 60/169,614  
<151> 1999-12-08

25 <160> 10

<170> FastSEQ for Windows Version 3.0

30 <210> 1  
<211> 3219  
<212> DNA  
<213> Arabidopsis thaliana, MAPK4 genomic fragment

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<222> (1157) (1329)

40 <221> CDS  
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<222> (2399) (2582)

50 <221> CDS  
<222> (2655) (2824)

<400> 1

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aaaagagcta agacttggtt gtgaatatag aggaaacatg taattatggt atcgttgatg 180  
ttaagtaata acaaatgcay ataaaaatga gactttaaaa cgcttcaaatt attgataact 240  
ctctcttttc aatcggttyct aagctataac tacattttca agttagtcag aattgtgctt 300  
tagttcatct tagttgataa tggataagtg atgggtttgc ttgaggccca ttgtaaatca 360

This <sup>File</sup> WAS  
SAVED in  
Acrobat,  
but  
cannot  
be processed  
in CRF.

Please see  
item # 4  
on error  
summary  
sheet.